



**UNITED STATES DEPARTMENT OF COMMERCE  
Patent and Trademark Office**

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Washington, D.C. 20231

008

09/300,425

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/300,425	04/28/99	NERI	113000.301

HM22/0801  
MILLEN, WHITE, ZELANO & BRANIGAN  
ARLINGTON COURTHOUSE PLAZA 1  
2200 CLARENDON BLVD, SUITE 1400  
ARLINGTON VA 22201

EXAMINER	
ART UNIT	PAPER NUMBER
	12

DATE MAILED: 1645

08/01/00

Please find below a communication from the EXAMINER in charge of this application.

Commissioner of Patents

*See Attached.*


Art Unit: 1645

*Sequence Letter*

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821 (a) (1) and (a) (2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.
2. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.136. In no case may and applicant extend the period of response beyond the six month statutory period and the response period is the time set in this action. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.
3. Please see attached Raw Sequence Listing Error Report.
- 4.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ginny Portner whose telephone number is (703)308-7543. The examiner can normally be reached on Monday through Friday from 7:30 AM to 5:00 PM except for the first Friday of each two week period.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith, can be reached on (703) 308-3909. The fax phone number for this group is (703) 308-4242.

  
**LYNETTE R. F. SMITH**  
**SUPERVISORY PATENT EXAMINER**  
**TECHNOLOGY CENTER 1600**

Art Unit: 1645

The Group and/or Art Unit location of your application in the PTO will be Group Art Unit 1645. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to this Art Unit.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Vgp

7/29/00

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Dario Neri  
Lorenzo Tarli  
Francesca Viti  
Manfred Birchler

Does Not Comply  
Corrected Diskette Needed

(ii) TITLE OF INVENTION: *more up - all response must be on*

SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES  
CONTAINING THEM AND THERAPEUTIC METHOD OF TREATMENT  
OF ANGIOGENESIS

*same line or  
leading*

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: PEPPER HAMILTON LLP  
(B) STREET: 600 Fourteenth Street, N.W.  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: U.S.A.  
(F) ZIP: 20005-2004

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy Disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC Windows  
(D) SOFTWARE: WP 8.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:  
(B) FILING DATE: April 28, 1999

(A) ~~(C) PRIOR APPLICATION: US 09/075,338~~

(B) ~~(D) PRIOR APPLICATION FILING DATE: May 11, 1998~~

~~(E) CLASSIFICATION:~~

(viii) ATTORNEY/AGENT INFORMATION: *colon*

- (A) NAME: Pepper Hamilton LLP  
(B) REGISTRATION NUMBER: 021269  
(C) REFERENCE/DOCKET NUMBER: 113000.301

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (202) 220-1200  
(B) TELEFAX: (202) 220-1665

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24  
(B) TYPE: ~~DNA~~ *nucleic acid*  
(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:  
(B) LOCATION:

(D) ~~(C) OTHER INFORMATION:~~

Description of Artificial Sequence: PCR primer: LMB1bis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

*use upper-case letters for bases, when using "old" format*  
ggggcccgag cggccatgac cgag

24

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54  
(B) TYPE: DNA  
(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:

*follow example  
shown above for  
subsequent sequences*

*This "mixed" sequence  
listing of "old" sequence rules  
format and "new" sequence rules  
format is invalid and  
unacceptable. Either consistently  
use old format throughout  
(which can be done in this  
case,*

*(vii) PRIOR APPLICATION DATA: since  
prior  
application  
was filed  
before 7/1/98,  
I use  
new format  
throughout.*

*(C) STRANDEDNESS: (mandatory leading  
(D) TOPOLOGY: and response needed)*

*If you decide to  
use new sequence  
rules format in  
corrected sequence listing,  
follow example shown  
in sample sequence  
listing (attached in back)*

If new sequence Pub format is used  
in connected sequence listing,  
please explain what residues "n's"  
represent, in C2207-L2237  
section

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(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DP47CDR1for

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

gagcctggcg gaccagctc atnnnnnnnnnctaaaggt gaatccagag gctg 54

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23

(B) TYPE: DNA

(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DP47CDR1back

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

atggcgtggg tccgccagcg tcc 23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60

(B) TYPE: DNA

(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DP47CDR2for

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

gtctgcgtag tatgtgtac cmnnactacc mnnaatmnnt gagaccact ccagcccctt 60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: DNA

(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DP47CDR2back

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

acatactacg cagactccgt gaag 24

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53

(B) TYPE: DNA

(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: JforNot

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

tcattctga ctgcggcgg cttgatttc caccttggtc ccttgccga acg 53

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

Edut  
=  
rest of  
sequence  
listing

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- (A) LENGTH: 47
- (B) TYPE: DNA
- (C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DPKCDR1for

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

gtttctgctg gtaccagctt aamngctgc tgctaacact ctgactg 47

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: DNA
- (C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DPKCDR1back

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ttagcctggt accagcagaa acc 23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46
- (B) TYPE: DNA
- (C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DPKCDR2for

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

gccagtggcc ctgctggatg cmnnatagat gaggagcctg ggagcc 46

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: DNA
- (C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DPKCDR2back

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

gcacccagca gggccactgg c 21

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45
- (B) TYPE: DNA
- (C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) OTHER INFORMATION:

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Description of Artificial Sequence: PCR primer: DP47baNco

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

gcggcccgagc atgcatggc cgaggtgcag ctgttgagc ctggg 45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55

(B) TYPE: DNA

(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: CDR3for

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

gggtccctgg cccagtagt caaamnnnnn nnnnnntttc gcaagtagt atacc 55

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: DNA

(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: VHpullth

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

gcggcccgagc atgcatggc cgag 24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66

(B) TYPE: DNA

(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: Jassm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

cccgctaccg ccaatggacc catcgccact cgagacggcg accaggggtc cctggcccca 60  
gtagtc 66

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62

(B) TYPE: DNA

(C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DPK22assm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

gatgggtcca gtggcggtag cggggcgcg tcgactggcg aaattgtgtt gacgcagtct 60  
cc 62

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 63
- (B) TYPE: DNA
- (C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: DPK3for

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

caccttggtc ccttggccga acgtmnnccg mnmnnaccm nncgtgctgac agtaatacac 60  
tgc 63

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56
- (B) TYPE: DNA
- (C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: Jfornot

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

gagtcattct cgacttgccg ccgctttgat ttccaccttg gtccttggc cgaacg 56

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: DNA
- (C) ORGANISM: ARTIFICIAL SEQUENCE

(ii) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) OTHER INFORMATION:

Description of Artificial Sequence: PCR primer: VLpullth

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

gatgggtcca gtggcggtag cggg 24

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116
- (B) TYPE: ~~PRT~~ amino acid
- (C) ~~ORGANISM:~~ (D) TOPOLOGY: *← mandatory leading and reverse*

~~VH antibody specific for ED-B domain of fibronectin~~

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1			5					10						15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Phe	
			20					25					30			
Ser	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
			35				40					45				
Ser	Ser	Ile	Ser	Gly	Ser	Ser	Gly	Thr	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	
			50			55				60						
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70				75					80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			
Ala	Lys	Pro	Phe	Pro	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	
			100					105								
Thr	Val	Ser	Ser													
			115													

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:



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(A) LENGTH: 14

(B) TYPE: ~~PRT~~ *amino acid*

(C) ORGANISM: ~~ANTIBODY LINKER~~

(D) TOPOLOGY: *← mandatory leading and sequence*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Asp Gly Ser Ser Gly Gly Ser Gly Gly Ala Ser Thr Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108

(B) TYPE: ~~PRT~~

(C) ORGANISM: *(D) TOPOLOGY: ←*

~~VL Antibody Specific for ED-B domain of Fibronectin~~

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: *(1) → 21*

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Tyr	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55				60					
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75				80	
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Thr	Gly	Arg	Ile	Pro
			85					90						95	
Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys				
			100					105							

## Appendix A To Subpart G to Part 1—Sample Sequence Listing

&lt;110&gt; Smith, John

Smith, Jane

## &lt;120&gt; Example of a Sequence Listing

&lt;130&gt; 01-00001

&lt;140&gt; US 08/999,999

&lt;141&gt; 1998-02-28

&lt;150&gt; EP 91000000

&lt;151&gt; 1997-12-31

Consult if you decide to use  
new format

<160> 2

<170> PatentIn ver. 2.0

<210> 1

<211> 403

<212> DNA

<213> Paramecium aurelia

<220>

<221> CDS

<222> 341..394

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a

Protease from Paramecium sp.

<303> Journal of Fictional Genes

<304> 1

<305> 4

<306> 1 - 7

<307> 1988-06-20

<400> 1

ctactctact ctactctcat ctactatctt ctttgatct ctgagtctgc ctgagtggta 60

ctcttgagtc ctggagatct ctctctcac atgtgatcgt cgagactgac cgatagatcg 120

ctgactgact ctgagatagt cgagcccgtta cgagaccgtt cgaggggtgac agagagtggg 180

cgcggtgcgcg cagagcgccg cgccggtgcg cgcgcgagtg cgcggtgggc cgcgcgaggg 240

ctttcgcggc agcgggcgcg ctttcggcg cgcgcccgtc cgcccctaga cctgagaggt 300

cttctcttcc ctctcttca ctagagaggt ctatatatac atg gtt tca atg ttc 355

Met Val Ser Met Phe

agc ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgtttgcgc 403

Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val

10

15

<210> 2

<211> 18

<212> PRT

<213> Paramecium aurelia

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu

1

5

10

15

Phe Val

ed: May 22, 1998.

A. Lehman,

ant Secretary of Commerce and

issioner of Patents and Trademarks.

oc. 98-14194 Filed 5-29-98; 8:45 am]

1 CODE 3510-16-C

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified



		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm- dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

# NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 C.F.R. 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

## Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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